```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=12; day=17; hr=11; min=8; sec=3; ms=26; ]
============================================================


************************************************************
Reviewer Comments:
<210>   10
<211>   519
<212>   PRT
<213>   Physcomitrella patens

<400>   10
Met Thr Ser Thr Glu Asn Thr Ala Met Phe Thr Glu Asp Thr Ser Thr
1               5                   10                  15
Leu Asn Gly Ser Thr Glu Ala Asn His Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
Arg Pro Thr Ile Gly Pro Glu Pro Pro Val Asn Pro Phe His Glu Ser
        35                  40                  45
Ser Thr Trp Ser Ile Pro Gln Val Ile Lys Thr Ile Leu Leu Val Pro
    50                  55                  60
Leu Leu Val Ile Arg Leu Leu Ser Met Phe Ala Leu Met Met Leu Gly
65                  70                  75                  80
Tyr Ile Cys Val Lys Val Ala Met Ile Gly Cys Lys Asp Pro Leu Phe
                85                  90                  95
Lys Pro Phe Asn Pro Leu Arg Arg Leu Leu Leu Val Ser Val Arg Leu
            100                 105                 110
Ile Ala Arg Gly Val Met Val Ala Met Gly Tyr Tyr Tyr Ile Leu Val
        115                 120                 125
Lys Gly Lys Pro Ala His Arg Ser Val Ala Pro Ile Ile Val Ser Asn
    130                 135                 140
His Ile Gly Phe Val Asp Pro Ile Phe Val Phe Tyr Arg His Leu Pro
145                 150                 155                 160
Val Ile Val Ser Ala Lys Glu Ile Val Glu Met Pro Ile Ile Gly Met
                165                 170                 175
Phe Leu Gln Ala Leu Gln Ile Ile Pro Val Asp Arg Ile Asn Pro Ala
```

```
            180                185                  190
Ser Arg His His Ala Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn
        195                200                  205
Glu Trp Pro His Val Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly
```

In the above attachment, please delete the extra space between the bases. This type of error is seen globally throughout the sequences in the sequence listing.

```
<210>  56
<211>  17752
<212>  DNA


<213>  Artificial sequence

<220>
<223>  Vector comprising genes coding for Physcomitrella patens Delta-6-
elongase, Physcomitrella patens Delta-6-desaturase, and Phaeodactylum
tricornutum Delta-5-desaturase
```

Invalid Line Length in Numeric Identifier <223>, The rules require that a line not exceed 72 characters in length. This includes white spaces. Please check for similar errors and make necessary changes.
****

Application No:	10552013	Version No:	3.0

Input Set:

Output Set:

Started:	2009-11-23 16:16:35.058
Finished:	2009-11-23 16:16:53.988
Elapsed:	0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings:	103
Total Errors:	202
No. of SeqIDs Defined:	148
Actual SeqID Count:	148

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (1)
W	402	Undefined organism found in <213> in SEQ ID (2)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (2)
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
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E	336	Empty lines found between the proteins and the dna

```
              Input Set:


              Output Set:


                Started:   2009-11-23 16:16:35.058
               Finished:   2009-11-23 16:16:53.988
                Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 930 ms
         Total Warnings:   103
           Total Errors:   202
   No. of SeqIDs Defined:  148
       Actual SeqID Count: 148


Error code     Error Description

E   355        Empty lines found between the amino acid numbering and the

E   321        No. of Bases conflict, this line has no nucleotides  SEQID (9)

E   300        Invalid codon found  Met SEQID  (9)   POS: 920

E   300        Invalid codon found  Leu SEQID  (9)   POS: 923

E   300        Invalid codon found  Phe SEQID  (9)   POS: 926

E   300        Invalid codon found  Pro SEQID  (9)   POS: 929

E   300        Invalid codon found  Glu SEQID  (9)   POS: 932

E   300        Invalid codon found  Gly SEQID  (9)   POS: 935

E   300        Invalid codon found  Thr SEQID  (9)   POS: 938

E   300        Invalid codon found  Thr SEQID  (9)   POS: 941

E   300        Invalid codon found  Thr SEQID  (9)   POS: 944

E   300        Invalid codon found  Asn SEQID  (9)   POS: 947

E   300        Invalid codon found  Gly SEQID  (9)   POS: 950

E   300        Invalid codon found  Lys SEQID  (9)   POS: 953

E   300        Invalid codon found  Ala SEQID  (9)   POS: 956

E   300        Invalid codon found  Leu SEQID  (9)   POS: 959

E   300        Invalid codon found  Ile SEQID  (9)   POS: 962

E   300        Invalid codon found  Ser SEQID  (9)   POS: 965

E   355        Empty lines found between the amino acid numbering and the

E   321        No. of Bases conflict, this line has no nucleotides  SEQID (11)

E   300        Invalid codon found  Lys SEQID  (11)  POS: 961

E   300        Invalid codon found  Ala SEQID  (11)  POS: 964
```

```
                    Input Set:


                    Output Set:



                    Started:   2009-11-23 16:16:35.058
                   Finished:   2009-11-23 16:16:53.988
                    Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 930 ms
            Total Warnings:    103
              Total Errors:    202
        No. of SeqIDs Defined: 148
          Actual SeqID Count:  148
```

Error code	Error Description
E 300	Invalid codon found Asn SEQID (11) POS: 967
E 300	Invalid codon found Gln SEQID (11) POS: 970 This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

```
                    Input Set:


                    Output Set:


                    Started:    2009-11-23 16:16:35.058
                   Finished:    2009-11-23 16:16:53.988
                    Elapsed:    0 hr(s) 0 min(s) 18 sec(s) 930 ms
            Total Warnings:     103
              Total Errors:     202
       No. of SeqIDs Defined:   148
           Actual SeqID Count:  148
```

Error code		Error Description
E	336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed
W	402	Undefined organism found in <213> in SEQ ID (37)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (48)
W	213	Artificial or Unknown found in <213> in SEQ ID (52)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W	213	Artificial or Unknown found in <213> in SEQ ID (53)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W	213	Artificial or Unknown found in <213> in SEQ ID (54)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W	213	Artificial or Unknown found in <213> in SEQ ID (55)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W	213	Artificial or Unknown found in <213> in SEQ ID (56)
W	213	Artificial or Unknown found in <213> in SEQ ID (60)
W	213	Artificial or Unknown found in <213> in SEQ ID (61)
W	213	Artificial or Unknown found in <213> in SEQ ID (62)
W	213	Artificial or Unknown found in <213> in SEQ ID (63)
W	213	Artificial or Unknown found in <213> in SEQ ID (64)

```
                    Input Set:


                    Output Set:



                      Started:   2009-11-23 16:16:35.058
                     Finished:   2009-11-23 16:16:53.988
                      Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 930 ms
               Total Warnings:   103
                 Total Errors:   202
        No. of SeqIDs Defined:   148
            Actual SeqID Count: 148
```

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (65)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W	213	Artificial or Unknown found in <213> in SEQ ID (66)
W	213	Artificial or Unknown found in <213> in SEQ ID (67)
W	213	Artificial or Unknown found in <213> in SEQ ID (68)
W	213	Artificial or Unknown found in <213> in SEQ ID (71)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (71)
W	213	Artificial or Unknown found in <213> in SEQ ID (75)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W	213	Artificial or Unknown found in <213> in SEQ ID (76)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W	213	Artificial or Unknown found in <213> in SEQ ID (77)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W	213	Artificial or Unknown found in <213> in SEQ ID (78)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W	213	Artificial or Unknown found in <213> in SEQ ID (79) This error has occured more than 20 times, will not be displayed
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)

```
                    Input Set:


                    Output Set:


                     Started:    2009-11-23 16:16:35.058
                    Finished:    2009-11-23 16:16:53.988
                     Elapsed:    0 hr(s) 0 min(s) 18 sec(s) 930 ms
             Total Warnings:     103
               Total Errors:     202
       No. of SeqIDs Defined:    148
          Actual SeqID Count:    148
```

Error code	Error Description
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (81)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (82)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (83)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (84)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (85)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (86)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (87)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (88)
E 224	`<220>`,`<223>` section required as `<213>` has Artificial sequence or Unknown in SEQID (89)

This error has occured more than 20 times, will not be displayed

gggcggtgtc cggccgttcg agcgcgtgga cgccaac atg agc gcg tgg acg agg   55
                                        Met Ser Ala Trp Thr Arg
                                          1   5

gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg   103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
            10   15   20

ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc   151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
        25   30   35

acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc   199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

```
              40                45                    50
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc       247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                    60                65                    70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg       295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                    75                80                85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac       343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                    90                95                   100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc       391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
          105               110               115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gcg ggc       439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Ala Gly
          120               125               130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct       487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135               140               145                   150
cct cga gat tcg tcg agc gag aag cac cac gcg ccg ctt ctt gtg          535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Leu Pro Leu Leu Val
                    155               160               165
ttc ccg gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag       583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
                    170               175               180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag       631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
          185               190               195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg       679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
          200               205               210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac       727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215               220               225                   230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag       775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                    235               240               245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg       823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
          250               255               260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc       871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
          265               270               275
gtc cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga          919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
          280               285               290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca     972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295               300               305
agcggtccag caacgggaga ttaaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa     1032
aaaaaaaaaa aaaaa                                                      1047




<210> 2
<211> 305
<212> PRT
<213> Thraustochytrium
```

<400> 2

Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
1   5   10   15

Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
            20   25   30

Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
        35   40   45

Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Val
    50   55   60

Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65   70   75   80

Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
                85   90   95

Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
            100   105   110

Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
        115   120   125

Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
    130   135   140

Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145   150   155   160

Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
                165   170   175

Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
                180   185   190

Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
        195   200   205

Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
    210   215   220

Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225   230   235   240

Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
                245   250   255

Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260   265   270

Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
    275   280   285

Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Asp Asp Leu
    290   295   300

Leu
305

<210> 3
<211> 1701
<212> DNA
<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 3
ggcacgaggg aaattggctt tctatgtggc cgtacttatt cgaggaggtc aacgaaacaa   60
aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc   120

```
aact gaaaac ttgttttaat tttttcttaa attgaaattc tgtgcctgaa agccaactct      180
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct      240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg      300
cttcacttca ttcttatgtc aatgaatgtc gtgatgaatc cggttaattc catcctacag      360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt      420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat      480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc      540
cttgtttggt tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt      600
ggatgctccc gtcatcaaga catacattga cagtttttcaa gataaaagag atcctctctg      660
gctagtcgtg ttcctgaagg cacagatttt ttcgtaaggc tgaagtaccc atccatggct      720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca      780
agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta      840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga      900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact      960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag    1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt    1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg    1140
ctgtatgatc tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct    1200
ttccctgaca gtggaattga agagagccct ttgaacatag tggaaggtgt ttgcaatgtt    1260
gctctacacg tagtccttag cggttgggta ttctggtgct tgtttcattc ggtttggttg    1320
aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga    1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt    1440
agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaagggtga ggctcctctt    1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta    1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgtatgtggcc ttttagcctt    1620
ctcctttacc catctgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc    1680
cccaaaaaaa aaaaaaaaa a                                              1701


<210>  4
<211>  714
<212>  DNA
<213>  Physcomitrella patens

<220>
<221>  CDS
<222>  (1)..(714)
<223>  LPAAT

<400>  4
atg gct ttg atg tat atc tgc aat ctt ctc tat aat ctg cat tta ttc      48
Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                   10                  15

tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc      96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30

aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat     144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45

gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa     192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60

ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt     240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80

gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac     288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
```

```
                    85                  90                      95
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta      336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100                 105                 110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca      384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115                 120                 125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat      432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
    130                 135                 140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca      480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg      528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta      576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
                180                 185                 190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc      624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                 200                 205
gct agt ttg ctg cgg gtt agt acc tat ttt gat tgg aga cct aaa          672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210                 215                 220
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa             714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235


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Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                   10                  15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
                20                  25                  30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100                 105                 110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115                 120                 125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                 135                 140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
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Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
            180                 185                 190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Leu Tyr Val Ala Phe
        195                 200                 205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210                 215                 220
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235


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<213>  Physcomitrella patens


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acaatatgtg gtcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa     180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta     240
gataccctca caagtatgtc aacccctctt ggtgtgacca aggaggtccg ttggtcgttg     300
tgttcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga     360
agccaactgt gagagagatg aaataccctc atgaatcgc aagtagagtt cgcagcgaga     420
tggctaaagc gttaggcatc gtgtgcacag aacacagctt tctgatatt aagctagcgc     480
tggctgcaga aaagctcaaa cagcctt                                       507


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Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu
1               5                   10                  15
ctc aac ggg gtc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa      96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc     144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
        35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg     192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
    50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg     240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc     288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
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                85                    90                    95
ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cgg ttc      336
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